Applicants : John David Fraser, *et al.*
Serial No. : 10/594,291
Filed : July 18, 2007
Page : 3 of 13

Attorney Docket No.: 55502-012US1
Client Ref. No.: SHR 504430 USPR

AMENDMENTS TO CLAIMS

This listing of claims replaces all prior versions and listings of claims in the application:

Listing of claims

1. (Currently amended) A method of isolating IgA present in a sample, the method comprising at least the steps of :

[[B]]bringing a SET1 polypeptide or a functional equivalent thereof in contact with the sample for a period sufficient to allow the SET1 polypeptide or functional equivalent thereof to bind to IgA to form a complex;

[[S]]separating the complex; and,

[[R]]releasing IgA from the complex; wherein the SET1 polypeptide comprises (a) an amino acid sequence having at least 80% similarity to SEQ ID NO:1, or (b) a fragment of the amino acid sequence that lacks only a signal peptide sequence as compared to the amino acid sequence.

2. (Cancelled)

3. (Currently amended) A method for isolating IgA from a sample, the method comprising at least the steps of :

[[P]]providing a matrix to which a SET1 polypeptide protein or functional equivalent is bound;

[[P]]providing a sample;

[[B]]bringing said matrix and said sample into contact for a period sufficient to allow the SET1 polypeptide protein or functional equivalent thereof to bind to IgA present in the sample; and,

[[R]]releasing IgA from the matrix, wherein the SET1 polypeptide comprises (a) an amino acid sequence having at least 80% similarity to SEQ ID NO:1, or (b) a fragment of the amino acid sequence that lacks only a signal peptide sequence as compared to the amino acid sequence.

Applicants   :   John David Fraser, *et al.*
Serial No.   :   10/594,291
Filed   :   July 18, 2007
Page   :   4 of 13

Attorney Docket No.: 55502-012US1
Client Ref. No.: SHR 504430 USPR

4. (Original) A method as claimed in claim 3 wherein the method further comprises the step of collecting the IgA released.

5. (Previously presented) A method as claimed in claim 3 wherein the matrix is in the form of a column over which the sample is passed.

6. (Previously presented) A method as claimed in claim 3 wherein the method further comprises the step of washing contaminants present in the sample from the matrix prior to release of IgA.

7. (Previously presented) A method as claimed in claim 3 wherein the matrix is Sepharose.

8. (Previously presented) A method as claimed in claim 3 wherein the sample is milk.

9. (Previously presented) A method as claimed in claim 3 wherein the sample is colostrum.

10. (Previously presented) A method as claimed in claim 3 wherein the sample is serum.

11. (Previously presented) A method as claimed in claim 3 wherein the method further comprises the step of determining the quantity of IgA present in the sample.

12. (Previously presented) A method as claimed in claim 3 wherein IgA is released from the matrix using a 100mM glycine buffer at pH 3.0.

13-22. (Cancelled)

23. (Currently amended) A method of detecting IgA in a sample, the method comprising at least the steps of:

[[C]]contacting a sample with a SET1 polypeptide or functional equivalent thereof for a period sufficient to allow the SET1 polypeptide or functional equivalent thereof to bind to IgA; and,

[[D]]detecting bound SET1 polypeptide or functional equivalent thereof, wherein the SET1 polypeptide comprises (a) an amino acid sequence having at least 80% similarity to SEQ ID NO:1, or (b) a fragment of the amino acid sequence that lacks only a signal peptide sequence as compared to the amino acid sequence.

24. (Cancelled)

25. (Currently amended) A method as claimed in claim 23 wherein the method further includes the step of determining or quantifying the level of the bound SET1 polypeptide.

26. (Original) A method as claimed in claim 23 wherein the method is conducted for the purpose of diagnosing IgA abnormality in a subject.

27. (Cancelled)

28. (Previously presented) A method as claimed in claim 23 wherein the subject is a mammal.

29. (Original) A method as claimed in claim 28 wherein the mammal is a human.

Applicants	:	John David Fraser, *et al.*
Serial No.	:	10/594,291
Filed	:	July 18, 2007
Page	:	6 of 13

Attorney Docket No.: 55502-012US1
Client Ref. No.: SHR 504430 USPR

30. (Currently amended) A method of removing IgA from a sample, the method comprising at least the steps of:

[[B]]bringing a SET1 polypeptide or a functional equivalent thereof in contact with the sample for a period sufficient to allow the SET1 polypeptide or functional equivalent thereof to bind to IgA to form a complex; and,

[[S]]separating the complex from the sample, wherein the SET1 polypeptide comprises (a) an amino acid sequence having at least 80% similarity to SEQ ID NO:1, or (b) a fragment of the amino acid sequence that lacks only a signal peptide sequence as compared to the amino acid sequence.

31-37. (Cancelled)

38. (New) The method as claimed in claim 1, wherein the SET1 polypeptide comprises the fragment, which is a mature SET1 having the amino acid sequence selected from the group consisting of SEQ ID NO:6, SEQ ID NO:7, and SEQ ID NOs:14-18.

39. (New) The method as claimed in claim 38, wherein the SET1 polypeptide is a fusion protein containing the mature SET1.

40. (New) The method as claimed in claim 1, wherein the SET polypeptide comprises a precursor SET1 having the amino acid sequence selected from the group consisting of SEQ ID NOs:1 and 3-5.

41. (New) The method as claimed in claim 40, wherein the SET polypeptide is a fusion protein containing the precursor SET1.

42. (New) The method as claimed in claim 3, wherein the SET1 polypeptide comprises the fragment, which is a mature SET1 having the amino acid sequence selected from the group consisting of SEQ ID NO:6, SEQ ID NO:7, and SEQ ID NOs:14-18.

Applicants   :   John David Fraser, *et al.*
Serial No.   :   10/594,291
Filed   :   July 18, 2007
Page   :   7 of 13

Attorney Docket No.: 55502-012US1
Client Ref. No.: SHR 504430 USPR

43.   (New) The method as claimed in claim 42, wherein the SET1 polypeptide is a fusion protein containing the mature SET1.

44.   (New) The method as claimed in claim 3, wherein the SET polypeptide comprises a precursor SET1 having the amino acid sequence selected from the group consisting of SEQ ID NOs:1 and 3-5.

45.   (New) The method as claimed in claim 44, wherein the SET polypeptide is a fusion protein containing the precursor SET1 protein.

46.   (New) The method as claimed in claim 23, wherein the SET1 polypeptide comprises the fragment, which is a mature SET1 having the amino acid sequence selected from the group consisting of SEQ ID NO:6, SEQ ID NO:7, and SEQ ID NOs:14-18.

47.   (New) The method as claimed in claim 46, wherein the SET1 polypeptide is a fusion protein containing the mature SET1.

48.   (New) The method as claimed in claim 23, wherein the SET polypeptide comprises a precursor SET1 having the amino acid sequence selected from the group consisting of SEQ ID NOs:1 and 3-5.

49.   (New) The method as claimed in claim 48, wherein the SET polypeptide is a fusion protein containing the precursor SET1.

50.   (New) The method as claimed in claim 30, wherein the SET1 polypeptide comprises the fragment, which is a mature SET1 having the amino acid sequence selected from the group consisting of SEQ ID NO:6, SEQ ID NO:7, and SEQ ID NOs:14-18.

51.   (New) The method as claimed in claim 50, wherein the SET1 polypeptide is a fusion protein containing the mature SET1.

52.   (New) The method as claimed in claim 30, wherein the SET polypeptide comprises a precursor SET1 having the amino acid sequence selected from the group consisting of SEQ ID NOs:1 and 3-5.

53.   (New) The method as claimed in claim 52, wherein the SET polypeptide is a fusion protein containing the precursor SET1.